

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 14:35:04 ; Search time 2798 Seconds

(without alignments)  
9888.466 Million cell updates/sec

Title: US-10-627-141-14

Sequence: 1 TTCATACAGTACGCCCCAGC.....CTTACATCCCTGTAGTTC 571

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*

1: gb\_ba:\*

2: gb\_hlg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pac:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_srs:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	571	100.0	571	6	AR432668	AR432668 Sequence
2	567.8	99.4	571	6	AR432670	AR432670 Sequence
3	566.2	99.2	571	14	BDU58594	BDU58594 Borna disease
4	564.6	98.9	1112	6	AR098533	AR098533 Sequence
5	564.6	98.9	1112	6	AR108878	AR108878 Sequence
6	564.6	98.9	8909	14	BD1311521	BD1311521 Borna dis
7	564.6	98.9	8910	6	AR098546	AR098546 Sequence
8	564.6	98.9	8910	6	AR108891	AR108891 Sequence
9	564.6	98.9	8910	14	BDU04608	BDU04608 Borna disease
10	563	98.6	571	6	AR432669	AR432669 Sequence
11	563	98.6	571	6	BDU58596	BDU58596 Borna disease
12	561	98.2	8910	6	AR432655	AR432655 Sequence
13	560.6	98.2	571	6	AR432667	AR432667 Sequence
14	558.2	97.8	571	14	BDU58595	BDU58595 Borna disease
15	555	97.2	1110	14	BDU094867	BDU094867 Borna disease
16	553.4	96.9	8909	14	BD1311523	BD1311523 Borna dis
17	551.8	96.6	1110	14	BDU094863	BDU094863 Borna disease
18	551.8	96.6	3694	14	AY066023	AY066023 Borna dis
19	540.6	94.7	1110	14	BDU94875	BDU94875 Borna disease

20	540.6	94.7	1110	14	BDU94879	BDU94879 Borna disease
21	540.6	94.7	1118	14	BDV38K	BDV38K Borna disease
22	540.6	94.7	1133	14	BDVPOLYMER	BDVPOLYMER Borna disease
23	540.6	94.7	1851	14	SG2821	SG2821 p18-pulcrativ
24	540.6	94.7	8908	14	AY114161	AY114161 Borna dis
25	540.6	94.7	8908	14	AY114162	AY114162 Borna dis
26	540.6	94.7	8908	14	AY114163	AY114163 Borna dis
27	540.6	94.7	8908	14	BDV580	BDV580 Borna disease
28	540.6	94.7	8909	14	BD1311522	BD1311522 Borna dis
29	537.4	94.1	1113	14	AF158629	AF158629 Borna dis
30	531	92.0	1138	14	SG7502S1	SG7502 p40, p24 (B
31	529.4	92.7	1110	14	BDU94871	BDU94871 Borna disease
32	500.2	87.6	529	14	BD1246853	BD1246853 Borna dis
33	498.6	87.3	529	14	BD1246850	BD1246850 Borna dis
34	498.6	87.3	529	14	BD1246851	BD1246851 Borna dis
35	498.6	87.3	529	14	BD1246852	BD1246852 Borna dis
36	498.6	87.3	529	14	BD1246854	BD1246854 Borna dis
37	498.6	87.3	529	14	BD1246856	BD1246856 Borna dis
38	497	87.0	529	14	BD1246857	BD1246857 Borna dis
39	493.8	86.5	529	14	BD1246855	BD1246855 Borna dis
40	437.4	76.6	439	14	BDVPT1P40	BDVPT1P40 Borna disease
41	434.2	76.0	439	14	BDAP001613	BDAP001613 Borna dis
42	433.4	75.9	459	14	BD1250177	BD1250177 Borna dis
43	432.6	75.8	439	14	BDAP001615	BDAP001615 Borna dis
44	431	75.5	439	14	BDAP001610	BDAP001610 Borna dis
45	431	75.5	439	14	BDAP001616	BDAP001616 Borna dis

## ALIGNMENTS

RESULT 1	AR432668	571 bp	mRNA	linear	PAT 18-DEC-2003
LOCUS	Sequence 14 from patent US 6653464.				
DEFINITION	AR432668				
ACCESSION	AR432668.1	GI:40195247			
VERSION					
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 571)				
AUTHORS	de la Torre, V.C.				
TITLE	Methods and compositions for screening for human Borna disease virus				
JOURNAL	Patent: US 6653464-A 14 25-NOV-2003;				
FEATURES	location/Qualifiers				
source	1..571				
	/organism="unknown"				
	/mol_type="mRNA"				
ORIGIN					
Query Match	100.0%; Score 571; DB 6; Length 571;				
Best Local Similarity	100.0%; Pred. No. 6e-171;				
Matches 571; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	TTCATACAGTACGCGCCAGCTGTGTTCTATGTTCTATCCAGACGACGCTG	60		
DB	1	TTCATACAGTACGCGCCAGCTGTGTTCTATGTTCTATCCAGACGACGCTG	60		
QY	61	CGTTTGTTCACGAGGGGTGCTGTAATCTTACGCGGAAAGACGAGCGTGAAG	120		
DB	61	CGTTTGTTCACGAGGGGTGCTGTAATCTTACGCGGAAAGACGAGCGTGAAG	120		
QY	121	AACGACGTGTTAAGCTGCGAAGTTTACGCGGAAAGACGAGCGTGAATCTCA	180		
DB	121	AACGACGTGTTAAGCTGCGAAGTTTACGCGGAAAGACGAGCGTGAATCTCA	180		
QY	181	CCGAGCTGAGATCTCTCTATCTTACGCGCATTTGTTCTCTATTAAGAGGTTGGA	240		
DB	181	CCGAGCTGAGATCTCTCTATCTTACGCGCATTTGTTCTCTATTAAGAGGTTGGA	240		
QY	241	TGAGTCTGCTCTTAAGTCAAGACGAGCGCGAGACATCAAGAAAGTTTAAACTA	300		
DB	241	TGAGTCTGCTCTTAAGTCAAGACGAGCGCGAGACATCAAGAAAGTTTAAACTA	300		

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OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 11:37:54 ; Search time 422.333 Seconds  
(without alignments)  
8003.565 Million cell updates/sec

Title: US-10-627-141-14

Perfect score: 571

Sequence: 1 TTTCATACAGTACAGCCGAC.....CTTACATCCTGTAGTTGC 571

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq.16Dec04:\*

1: geneeqn19808:\*\n2: geneeqn19808:\*\n3: geneeqn20008:\*\n4: geneeqn2001as:\*\n5: geneeqn2001bs:\*\n6: geneeqn2002as:\*\n7: geneeqn2002bs:\*\n8: geneeqn2003as:\*\n9: geneeqn2003bs:\*\n10: geneeqn2003cs:\*\n11: geneeqn2003ds:\*\n12: geneeqn2004as:\*\n13: geneeqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	571	100.0	571	2	AAV32851 Human Bor
2	567.8	99.4	571	2	AAV32853 Human Bor
3	564.6	98.9	8910	2	AAV38104 Borna dis
4	563	98.6	571	2	AAV32852 Human Bor
5	537.4	94.1	1113	4	AAAF61225 Borna dis
6	448	78.5	559	4	AAAF61230 Borna dis
7	90.4	15.8	501	6	ABH36599 Human col
8	90.4	15.8	1047	4	AAH13875 Human col
9	90.4	15.8	1293	4	AAH161251 Human col
10	90.4	15.8	1293	10	AAH04080 Human CDN
11	90	15.8	721	4	AAH04080 Human CDN
12	88.8	15.6	1311	10	AAH07119 Novel cod
13	85.8	15.0	981	4	AAH59465 Novel pol
14	83.8	14.7	1626	12	ADDO0623 Novel hum
15	83.8	14.7	1626	12	ADDO0044 Novel hum
16	83.8	14.7	1626	12	ADN98875 Novel hum
17	83.8	14.7	1626	12	ADN98875 Novel hum
18	76.4	13.4	1665	12	ADEN9054 Novel hum
19	76.2	13.3	4940	10	ADP82143 Leukemia
20	76.2	13.3	4940	10	ADP82144 Leukemia

21	67.8	11.9	804	3	AACT7204
22	63.8	11.2	2843	4	AAH16588 Human CDN
23	60.6	10.6	712	6	ABT10107 Human bre
24	58.6	10.3	430	10	ADP80751
25	57.2	10.0	1557	12	ADJ84332 Human phe
26	56.6	9.9	466	12	ADP66154 Human CDN
27	56	9.8	767	4	AAI96380 Human neu
28	44.6	7.8	836	4	AAI96519 Human neu
29	39.8	7.0	2000	8	ADA71938 Human neu
30	34.4	6.0	672	10	ADB55214 Toxicity-
31	34.4	6.0	672	10	ADB49727 Primary r
32	33.8	5.9	250	3	AACT2730 Human sec
33	33.8	5.9	553	4	AAH13122 Human CDN
34	33.8	5.9	693	3	AAH75126 CDNA enco
35	33.6	5.9	588	4	AAH09586 Human CDN
36	32.8	5.7	4983	12	ADQ63005 Novel hum
37	32.4	5.7	4062	8	ADA71340 Rice gene
38	32.4	5.7	5642	5	AAK69744 Human imm
39	32.4	5.7	5642	5	AAK34694 Human DNA
40	32.2	5.6	3515	2	AAK20252 Borrelia
41	32.2	5.6	110000	6	ABQ69245_16 Continuation (17 o
42	32.2	5.6	709	4	AAK85690 Human imm
43	32	5.6	711	4	AAK85689 Human imm
44	32	5.6	711	4	AAK85689 Human imm
45	31.8	5.6	310	6	ABL70681 Corn tase

#### ALIGNMENTS

RESULT 1  
AAV32851 standard; CDNA; 571 BP.

AAV32851;

27-AUG-2003 (revised)  
09-NOV-1998 (first entry)

Human Borna disease virus p40 CDNA.

BDV; infection; diagnosis; neuropsychiatric disorder; human; ss.

Borna disease virus.

Key Location/Qualifiers  
CDS 3..569 /\*tag= a

MO9830238-A1.

16-JUL-1998.

07-JAN-1998; 98MO-US000495.

07-JAN-1997; 97US-00779764.

(SCRI) SCRIPPS RES INST.

De la Torre JC;

WPI; 1998-398802/34.  
P-PSDB; AAM49051.

New isolated human Borna disease nucleic acid(s) - which encode p24, p16, p56, p40 and L polymerase catalytic domain poly-peptide(s), used to develop products for detection.

Claim 13; Page 128; 207pp; English.

This CDNA sequence codes for p40 polypeptide (see AAM49051) of a Borna disease virus (BDV) isolate (HI) obtained from a psychiatric patient with a mood disorder. It can be produced by PCR (see also AAV32866-69) of CDNA





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OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 13:08:09 ; Search time 2654 Seconds

(without alignments)  
8189.411 Million cell updates/sec

Title: US-10-627-141-14

Sequence: 1 TTCAATACAGTACGCCACG.....CTTCAATCCCTGATGTC 571

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST:  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_hic:  
4: gb\_est3:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_gse1:  
9: gb\_gse2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	90.4	15.8	582	2	AM593371 hg13h11.x
C 2	90.4	15.8	1679	3	BC051316 Homo sapi
C 3	90.4	15.8	721	1	AU119718 Homo sapi
C 4	87.4	15.3	580	1	AI808337 w54f08.x
C 5	85.8	15.0	408	1	AA812109 cb40c08.x
C 6	77.8	13.6	661	6	CD705171 ES121698
C 7	76.4	13.4	685	5	BC006526 UI-H-EU0
C 8	76.4	13.4	1790	3	BC033624 Homo sapi
C 9	76.4	13.4	1826	4	BC032471 Homo sapi
C 10	76.2	13.3	389	4	BM698664 UI-E-DX1
C 11	76.2	13.3	500	1	AL599858
C 12	76.2	13.3	725	5	BO183041
C 13	76.2	13.3	737	6	CB993540 AGENCOURT
C 14	75.4	13.2	932	5	BR993506 UIO-MTC01
C 15	74.8	13.1	866	5	EX445843
C 16	72.6	12.7	774	8	AA001666
C 17	71.4	12.5	548	1	BR993506
C 18	69.6	11.5	964	4	AG227224 HS-2017 B
C 19	65.8	11.2	455	8	CG137776
C 20	64.2	11.2	443	5	CG137776
C 21	63.8	11.2	470	7	CG137776
C 22	63.8	11.2	479	6	CG137776
C 23	63.8	11.2	479	6	CG137776
C 24	63.8	11.2	480	6	CG137776

25	63.8	11.2	481	5	BO271452	1k14b03.y
26	63.8	11.2	595	5	CA948940	1q30c11.y
27	63.8	11.2	641	5	BU951096	1075g09.y
28	63.8	11.2	733	6	CA707788	UI-H-FT1.x
C 29	63.8	11.2	750	6	CA75717	1097d10.x
C 30	63.8	11.2	752	6	CA775929	1p01d07.x
C 31	63.8	11.2	778	6	CA776003	1097d10.y
C 32	63.8	11.2	781	6	CA778017	1p16h02.x
C 33	63.8	11.2	798	6	CA776148	1p01d07.y
C 34	63.8	11.2	1042	4	BM474332	1075g09.y
C 35	63.4	11.1	437	8	BS4247	1075g09.y
C 36	62.8	11.0	454	7	CA778310	1075g09.y
C 37	62.2	10.9	711	6	CA778310	1075g09.y
C 38	61.6	10.8	562	5	BO271156	1p16h02.y
C 39	61.6	10.8	593	5	BU076047	1k14b03.x
C 40	61.6	10.8	601	5	BO269772	1k14b03.x
C 41	61.6	10.8	615	5	BU952536	1075g09.x
C 42	61.6	10.8	709	6	CD237377	1075g09.x
C 43	60.6	10.6	712	1	AA875998	ob93b09.s
C 44	60.2	10.5	558	7	CK005159	AGENCOURT
C 45	58.8	10.3	438	1	AI830973	wj80f03.x

## ALIGNMENTS

RESULT 1  
AM593371/c  
LOCUS hg13h11.x1 Soares NFL T GBC SW Homo sapiens cDNA clone  
DEFINITION IMAGE:2945541 3' similar to SW:VP40\_BDV Q01552 40 KD PROTEIN. [2]  
SW:VP40\_BDV ; mRNA sequence.

ACCESSION AM593371.1 GI:7280629  
VERSION AM593371  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
TITLE Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: -40UP from G1pco  
High quality sequence atp01: 464.

## FEATURES

location/Qualifiers  
1..582

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2945541"  
/lab\_host="DH10B"  
/clone\_lib="Soares\_NFL\_T\_GBC\_S1"  
/note="Organ: pooled; Vector: pRTT3D-Pac (Pharmacia) with  
a modified polylinker; Site 1: Not I; Site 2: Eco RI;  
Equal amounts of plasmid DNA from three normalized  
libraries (fetal lung NBHL19W, testis NHT, and B-cell  
NCI CGAP GCB1) were mixed and as circles were made in  
vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from pools of 5,000 clones made  
from the same 3 libraries. The pools consisted of  
I.M.A.G.E. clones 297480-302087, 682632-687239,  
726408-728711, and 729096-731399. Subtraction by Bento  
Soares and M. Fatima Bonaldo.

## ORIGIN

Query Match

15.8%; Score 90.4; DB 2; Length 582;

Result No.	Score	Query Match	Length	DB	ID	Description
1	571	100.0	571	6	AR432669	AR432669 Sequence
2	566.2	99.2	571	6	AR432670	AR432670 Sequence
3	566.2	99.2	571	14	BDU56595	U58555 Borna disease
4	563	98.6	571	6	AR432668	AR432668 Sequence
5	561.4	98.3	571	14	BDU56596	U58556 Borna disease
6	560.6	98.2	571	6	AR432667	AR432667 Sequence
7	559.8	98.0	1112	6	AR098533	AR098533 Sequence
8	559.8	98.0	1112	6	AR108878	AR108878 Sequence
9	559.8	98.0	8909	14	BD1311521	BD1311521 Borna disease
10	559.8	98.0	8910	6	AR098646	AR098646 Sequence
11	559.8	98.0	8910	6	AR108891	AR108891 Sequence
12	558.2	98.0	8910	14	BDU04608	BDU04608 Borna disease
13	558.2	97.8	571	14	BDU56594	U58554 Borna disease
14	556.2	97.4	8910	6	AR432655	AR432655 Sequence
15	550.2	96.4	1110	14	BDU94867	BDU94867 Borna disease
16	548.6	96.1	8909	14	BD1311523	BD1311523 Borna disease
17	547	95.8	1110	14	BDU94863	BDU94863 Borna disease
18	547	95.8	3694	14	AY060022	AY060022 Borna disease
19	535.8	93.8	1110	14	BDU94875	BDU94875 Borna disease

20	535.8	93.8	1110	14	BDV94879	U94879 Borna disease
21	535.8	93.8	1113	14	BDV938K	X68392 Borna disease
22	535.8	93.8	1113	14	BDVPOLYMER	M99375 Borna disease
23	535.8	93.8	1851	14	S62821	S62821 p38-putative
24	535.8	93.8	8908	14	AY114161	AY114161 Borna disease
25	535.8	93.8	8908	14	AY114162	AY114162 Borna disease
26	535.8	93.8	8908	14	AY114163	AY114163 Borna disease
27	535.8	93.8	8908	14	BDVSEQ	L27077 Borna disease
28	535.8	93.8	8909	14	BDJ11522	AJ115522 Borna disease
29	535.6	93.3	1113	14	AF158629	AF158629 Borna disease
30	526.2	92.2	1138	14	S6750281	S67502 p40, p24 1B
31	526.6	91.9	1110	14	BDV94871	U94871 Borna disease
32	495.4	86.8	529	14	BDJ246853	AJ246853 Borna disease
33	493.8	86.5	529	14	BDJ246850	AJ246850 Borna disease
34	493.8	86.5	529	14	BDJ246851	AJ246851 Borna disease
35	493.8	86.5	529	14	BDJ246852	AJ246852 Borna disease
36	493.8	86.5	529	14	BDJ246854	AJ246854 Borna disease
37	493.8	86.5	529	14	BDJ246856	AJ246856 Borna disease
38	493.8	86.5	529	14	BDJ246857	AJ246857 Borna disease
39	489	85.6	529	14	BDJ246855	AJ246855 Borna disease
40	432.6	75.8	439	14	BDVFT1P40	X84691 Borna disease
41	429.4	75.2	439	14	BDVAF001613	AF001613 Borna disease
42	428.6	75.1	439	14	BDJ250177	AF250177 Borna disease
43	427.8	74.9	439	14	BDVAF001615	AF001615 Borna disease
44	426.2	74.6	439	14	BDVAF001610	AF001610 Borna disease
45	426.2	74.6	439	14	BDVAF001616	AF001616 Borna disease

## ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	ORIGIN
AR432669	AR432669	Sequence 15 from patent US 6653464.	AR432669	AR432669.1	GI:40195248	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 571)	Methods and compositions for screening for human Borna disease virus	Patent: US 6653464-A 15 25-NOV-2003;	Location/Qualifiers	1..571
												/organism="unknown"	/mol_type="mRNA"

Query Match	100.0%	Score 571	DB 6	Length 571
Best Local Similarity	100.0%	Pred. No. 66-176		
Matches 571	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	TTCTATACAGTAAAGCCAGCCTTGCTGTTCATGTTCATGTTCATATCCAGAGCTGACGCTG	60	
Db	1	TTCTATACAGTAAAGCCAGCCTTGCTGTTCATGTTCATATCCAGAGCTGACGCTG	60	
QY	61	CGTTTGTTCAACGAGGGGTGCTTCGTAAATCTTAACCTGTGACGCGCTTATCAGCGGTGAG	120	
Db	61	CGTTTGTTCAACGAGGGGTGCTTCGTAAATCTTAACCTGTGACCGCTTATCAGCGGTGAG	120	
QY	121	AACAGACTGTGTTAAAGACTGCGAGTCTTAAACGGGGAAAAGACAGCAGAGGTGATCTCA	180	
Db	121	AACAGACTGTGTTAAAGACTGCGAGTCTTAAACGGGGAAAAGACAGCAGAGGTGATCTCA	180	
QY	181	CCGAGCTGGAGATCTCTCTATCTTCAGCCATTGTCTCATTAAGTAATAGGGGTGTGGA	240	
Db	181	CCGAGCTGGAGATCTCTCTATCTTCAGCCATTGTCTCATTAAGTAATAGGGGTGTGGA	240	
QY	241	TAGATATGTCGTCTAAGATCAAAAGCAGAACCCAGCAGATCAAGAAAAGGTTTAAACTA	300	

OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 11:37:54 ; Search time 422.333 Seconds

8003.565 Million cell updates/sec

Title: US-10-627-141-15  
Perfect score: 571

sequence: 1 TTCATACAGTAACGCCAGC.....CTTACAATCCCTGTAGTGC 571

scoring table: IDENTITY\_NTUC

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length:	0
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Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%

### Listing first 45 summaries

Database : N\_GeneSeq\_16Dec04:\*

1: geneseqn1990as: \*  
2: geneseqn1980as: \*  
3: geneseqn2000bs: \*  
4: geneseqn2001as: \*  
5: geneseqn2001bs: \*  
6: geneseqn2002as: \*  
7: geneseqn2002bs: \*  
8: geneseqn2003as: \*  
9: geneseqn2003bs: \*  
10: geneseqn2003cs: \*  
11: geneseqn2004as: \*  
12: geneseqn2004bs: \*  
13: geneseqn2004bs: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
1	571	100.0	571	2	AAV32852	AAV32852 Human Bor	
2	566.2	99.2	571	2	AAV32853	AAV32853 Human Bor	
3	563	98.6	571	2	AAV32851	AAV32851 Human Bor	
4	559.8	98.0	8910	2	AAV38104	AAV38104 Borra dis	
5	532.6	93.3	1113	4	AAFE1225	AAFE1225 Borra dis	
6	443.2	77.6	559	4	AAFE1230	AAFE1230 Borra dis	
7	88.8	15.6	501	6	ABEL3659	Human col	
8	88.8	15.6	1047	4	AAH13875	AAH13875 Human CDN	
9	88.8	15.6	1293	4	AAH161251	AAH161251 Human pol	
10	88.8	15.6	1293	10	ADBE08868	ADBE08868 Novel DNN	
11	88.4	15.5	721	4	AAH04080	AAH04080 Human cod	
12	87.2	15.3	1311	10	ADBE07119	ADBE07119 Novel cod	
13	84.2	14.7	981	4	AA159465	AA159465 Human pol	
14	82.2	14.4	1636	12	ADDO06623	ADDO06623 Novel hum	
15	82.2	14.4	1636	12	ADDO00444	ADDO00444 Novel hum	
16	82.2	14.4	1636	12	ADON98875	ADON98875 Novel hum	
17	82.2	14.4	1636	12	ADON99054	ADON99054 Novel hum	
18	76.2	13.3	1665	10	ADDES3865	ADDES3865 Human ptc	
19	76.2	13.3	4940	10	ADFE82143	ADFE82143 Leukemia	
20	76.2	13.3	4940	10	ADFE82144	ADFE82144 Leukemia	

21	66.2	11.6	804	3	AACT7204	Aac77204 Human ORF
22	63.8	11.2	2843	6	AAHI6588	AaI16588 Human CDN
23	60	10.5	712	6	ABT10107	ABt10107 Human bre
24	58.6	10.3	430	10	ADBF08751	Adf08751 Leukaemia
25	57.2	10.0	1557	12	ADJ84332	Adj84332 Human phi
26	56.6	9.9	466	12	ADP66154	Adp66154 Human CDN
27	56	9.8	767	4	AAI96380	AaI96380 Human CDN
28	45.8	8.0	836	4	AAI196519	AaI196519 Human neu
29	37.6	6.6	672	10	ADBS55214	Adbs55214 Toxicity
30	37.6	6.6	672	10	ADBA9727	Adba9727 Primary r
31	37.4	6.5	2000	8	ADA71938	Ada71938 Rice gene
32	35.4	6.2	110000	6	ABO63245_16	Continuation (17 o
33	35.4	6.2	110000	6	ABO67195_1	Continuation (12 o
34	33.8	5.9	250	3	AACT27230	Aac27230 Human sec
35	33.8	5.9	553	4	AAH13122	AaH13122 Human CDN
36	33.8	5.9	693	3	AAAT75126	Aaa75126 CDNA enco
37	33.8	5.9	35515	2	AAAT20252	Aaa20252 Human CDN
38	33.6	5.9	588	4	AAH09596	AaH09596 Botrelia
39	33.2	5.8	349980	5	AAH86431	AaH86431 Human CDN
40	32.8	5.7	4983	12	ADQ63005	Adq63005 Novel hum
41	32.6	5.7	181257	12	ADFP69677	Adfp69677 Human SLC
42	32.4	5.7	4062	8	ADA71340	Ada71340 Rice gene
43	32.4	5.7	5642	4	AAK69744	Aak69744 Human imm
44	32.4	5.7	5642	5	AAK34694	Aak34694 Human DNA
45	32.2	5.6	883	2	AAK20351	Aak20351 Botrelia

## ALIGNMENTS

RESULT 1  
AAV32852  
ID AAV32852 standard; cDNA; 571 BP.

AC AAV32852

DT 27-AUG-2003 (revised)

03-NOV-1996 (first entry)

DE Human Borna disease virus p40 cDNA.  
XX

BDV; infection; diagnosis; neuropsychiatric disorder; human; ss.

OS Borna disease virus.

FH	Key	Location/Qualifiers
1		

FT

PN WO9830238-A1

16-JUL-1998

XX 07-JAN-1988. 08WQ Y1C000040C  
PF

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XX : 3 4 5 6 7 8 9

DR WPL: 1998-398802/34  
DR P-PSDB: AAW49052

XX  
DT  
New isolated human E

PT p56, p40 and L polymerase catal

2

XX

virus sequence codes for p40 polypeptide (see AAM49052) of a Borna disease virus (BDV) isolate from a psychiatric patient with

CC a mood disorder. It can be produced by PCR (see also AAV32866-69) of cDNA

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 14:41:19 ; Search time 130.667 Seconds  
(without alignments)  
7150.362 Million cell updates/sec

Title: US-10-627-141-15

Perfect score: 571

Sequence: 1 TTCAATACAGTACGCCAGC.....CTTACATCCCTGTAGTTGC 571

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	571	100.0	571	US-09-563-456-15	Sequence 15, Appl
3	566.2	99.2	571	US-08-779-764A-16	Sequence 16, Appl
4	566.2	99.2	571	US-09-563-456-16	Sequence 16, Appl
5	563	98.6	571	US-08-779-764A-14	Sequence 14, Appl
6	563	98.6	571	US-09-563-456-14	Sequence 14, Appl
7	560.6	98.2	571	US-08-779-764A-13	Sequence 13, Appl
8	560.6	98.2	571	US-09-563-456-13	Sequence 13, Appl
9	559.8	98.0	1112	US-08-369-822C-1	Sequence 1, Appl
10	559.8	98.0	1112	US-08-582-776C-1	Sequence 1, Appl
11	559.8	98.0	1112	US-08-434-831B-1	Sequence 1, Appl
12	559.8	98.0	8910	US-08-369-822C-19	Sequence 19, Appl
13	559.8	98.0	8910	US-08-582-776C-19	Sequence 19, Appl
14	559.8	98.0	8910	US-08-434-831B-19	Sequence 19, Appl
15	556.2	97.4	8910	US-08-779-764A-1	Sequence 1, Appl
16	556.2	97.4	8910	US-09-563-456-1	Sequence 1, Appl
17	556.2	97.4	29935	US-09-949-016-11871	Sequence 11871, A
18	34	6.0	29936	US-09-949-016-14443	Sequence 14443, A
19	33.8	5.9	250	US-09-513-999C-31305	Sequence 31305, A
20	33.8	5.9	399	US-09-621-976-8976	Sequence 8976, Ap
21	33.2	5.8	601	US-09-949-016-52358	Sequence 52358, A
22	33.2	5.8	36156	US-09-949-016-12128	Sequence 12128, A
23	33.2	5.8	36156	US-09-949-016-13261	Sequence 13261, A
24	32.8	5.7	601	US-09-949-016-52357	Sequence 52357, A
25	32.8	5.7	601	US-09-949-016-52359	Sequence 52359, A
26	30.8	5.4	567	US-09-244-805-17	Sequence 17, Appl
27	30.6	5.4	1077	US-09-270-767-13644	Sequence 13644, A

28	30.6	5.4	1524	US-09-270-767-13500	Sequence 13500, A
29	30.6	5.4	83617	US-09-949-016-12254	Sequence 12254, A
30	30.4	5.3	4352	US-09-620-312D-555	Sequence 555, App
31	30.2	5.3	1422	US-09-270-767-12311	Sequence 12311, A
32	30.2	5.3	46347	US-09-949-016-13469	Sequence 13469, A
33	30	5.3	930	US-09-248-796A-8265	Sequence 8265, Ap
34	30	5.3	4291	US-09-351-200-1	Sequence 1, Appl
35	30	5.3	25733	US-09-902-540-1215	Sequence 1215, Ap
36	30	5.3	260247	US-09-949-016-13358	Sequence 13358, A
37	29.8	5.2	265	US-09-313-294A-3339	Sequence 3339, Ap
38	29.8	5.2	291	US-09-313-294A-6731	Sequence 6731, Ap
39	29.8	5.2	297	US-09-313-294A-4410	Sequence 4410, Ap
40	29.8	5.2	417	US-09-134-000C-3173	Sequence 3173, Ap
41	29.8	5.2	417	US-09-134-000C-3175	Sequence 3175, Ap
42	29.8	5.2	492	US-09-248-796A-13868	Sequence 13868, A
43	29.8	5.2	3789	US-09-107-433-2464	Sequence 2464, Ap
44	29.6	5.2	519	US-09-270-767-7501	Sequence 7501, Ap
45	29.6	5.2	519	US-09-270-767-22783	Sequence 22783, A

## ALIGNMENTS

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RESULT 1
US-08-779-764A-15
Sequence 15, Application US/08779764A
Patent No. 6057094
GENERAL INFORMATION:
APPLICANT: de la Torre, Juan C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
TITLE OF INVENTION: OF HUMAN BORNA DISEASE VIRUS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESS: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10550 No. 6057094th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: United States
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779, 764A
FILING DATE: 16-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 465.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 571 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-779-764A-15
Query Match 100.0%; Score 571; DB 3; Length 571;
Best Local Similarity 100.0%; Pred. No. 2.6e-196;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 TTCAATACAGTACGCCAGCCTTGTGTTCTATGTTGCTAATCCAGAGCTGCAGCGTG 60
1 TTCAATACAGTACGCCAGCCTTGTGTTCTATGTTGCTAATCCAGAGCTGCAGCGTG 60
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 17:28:54 ; Search time 463 Seconds  
(without alignments)  
7464.304 Million cell updates/sec

Title: US-10-627-141-15

Perfect score: 571  
Sequence: 1 TTCATACAGTACGCCAGC.....CTTACATCCCTGATGTC 571

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 5607317 seqs, 3026245999 residues

Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications\_NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
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- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*
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- 22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	571	100.0	571	18	US-10-627-141-15
2	566.2	99.2	571	18	US-10-627-141-16
3	563	98.6	571	18	US-10-627-141-14
4	560.6	98.2	571	18	US-10-627-141-13
5	556.2	97.4	8910	18	US-10-627-141-11
6	88.8	15.6	498	9	US-09-878-178-188
7	88.8	15.6	498	13	US-10-046-935-188
8	88.8	15.6	498	14	US-10-146-502-188
9	88.8	15.6	1293	18	US-10-128-558-288
10	87.2	15.3	1311	18	US-10-128-558-61
11	76.2	13.3	1665	16	US-10-252-157-212

12	58.4	10.2	1557	13	US-10-027-632-260709	Sequence 260709,
13	58.4	10.2	1557	17	US-10-027-632-260709	Sequence 260709,
14	57.2	10.0	1557	13	US-10-027-632-260704	Sequence 260704,
15	57.2	10.0	1557	13	US-10-027-632-260704	Sequence 260704,
16	57.2	10.0	1557	13	US-10-027-632-260705	Sequence 260705,
17	57.2	10.0	1557	13	US-10-027-632-260706	Sequence 260706,
18	57.2	10.0	1557	13	US-10-027-632-260707	Sequence 260707,
19	57.2	10.0	1557	13	US-10-027-632-260708	Sequence 260708,
20	57.2	10.0	1557	17	US-10-027-632-260703	Sequence 260703,
21	57.2	10.0	1557	17	US-10-027-632-260705	Sequence 260705,
22	57.2	10.0	1557	17	US-10-027-632-260706	Sequence 260706,
23	57.2	10.0	1557	17	US-10-027-632-260707	Sequence 260707,
24	57.2	10.0	1557	17	US-10-027-632-260708	Sequence 260708,
25	57.2	10.0	1557	17	US-10-027-632-260709	Sequence 260709,
26	56.6	9.9	466	18	US-10-637-855-146	Sequence 146, App
27	35.4	6.2	495269	17	US-10-398-221-8	Sequence 8, Appl
28	35.4	6.2	3011208	17	US-10-398-221-2058	Sequence 2058, Ap
29	34	6.0	121410	19	US-10-741-600-17733	Sequence 17733, A
30	33.4	5.8	305	17	US-10-242-535A-49642	Sequence 49642, A
31	33.4	5.8	305	17	US-10-085-783A-49642	Sequence 49642, A
32	33.4	5.8	1748	18	US-10-425-115-112215	Sequence 112215,
33	33.2	5.8	478	13	US-10-027-632-75475	Sequence 75475, A
34	33.2	5.8	478	13	US-10-027-632-109080	Sequence 109080,
35	33.2	5.8	478	17	US-10-027-632-75475	Sequence 75475, A
36	33.2	5.8	478	17	US-10-027-632-109080	Sequence 109080,
37	33.2	5.8	1323	13	US-10-027-632-251152	Sequence 251152,
38	33.2	5.8	1323	13	US-10-027-632-251152	Sequence 251152,
39	33.2	5.8	1323	17	US-10-027-632-251152	Sequence 251152,
40	33.2	5.8	1323	13	US-10-027-632-251154	Sequence 251154,
41	32.8	5.7	1323	13	US-10-027-632-251151	Sequence 251151,
42	32.8	5.7	1323	13	US-10-027-632-251153	Sequence 251153,
43	32.8	5.7	1323	17	US-10-027-632-251151	Sequence 251151,
44	32.8	5.7	1323	17	US-10-027-632-251153	Sequence 251153,
45	32.8	5.7	4483	18	US-10-437-963-8503	Sequence 8503, Ap

#### ALIGNMENTS

RESULT 1  
US-10-627-141-15  
Sequence 15, Application US/10627141  
Publication No. US20040162421A1  
GENERAL INFORMATION:  
APPLICANT: de la Torre, Juan C.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING  
OF HUMAN BORNA DISEASE VIRUS  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE  
STREET: 10550 North Torrey Pines Road, TPC-8  
CITY: La Jolla  
STATE: California  
COUNTRY: United States  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/627,141  
FILING DATE: 25-Jul-2003  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/779,764  
FILING DATE: 16-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSRI 465.0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 784-2937

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OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 13:08:09 ; Search time 2654 Seconds  
(without alignments)  
8189.411 Million cell updates/sec

Title: US-10-627-141-15

Perfect score: 571  
Sequence: 1 TTCAATACAGTAACGCCACG.....CTTAAATCCTGTAATTGC 571

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST: \*  
1: gb\_esc1: \*  
2: gb\_esc2: \*  
3: gb\_hc: \*  
4: gb\_esc3: \*  
5: gb\_esc4: \*  
6: gb\_esc5: \*  
7: gb\_esc6: \*  
8: gb\_gss1: \*  
9: gb\_gss2: \*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	88.8	15.6	582	2	AM593371 hg13h11.x
C 2	88.8	15.6	1679	3	BC051316 Homo sapi
C 3	88.8	15.5	721	1	AU119718 AU119718
C 4	85.8	15.0	580	1	AI808337 v554f08.x
C 5	84.2	14.7	408	1	AA812109 CD705171
C 6	77.8	13.6	661	6	CD705171 EST21698
C 7	76.4	13.4	389	4	BQ006526 UI-H-E-D11-
C 8	76.2	13.3	685	4	BM698664 UI-E-DX1-
C 9	76.2	13.3	500	1	AL599858 DKF2313C
C 10	76.2	13.3	725	5	BO183041 UI-H-EUO-
C 11	76.2	13.3	737	6	CB993540 ACENCOURT
C 12	76.2	13.3	1790	3	BC033624 Homo sapi
C 13	76.2	13.3	1826	3	BC032471 Homo sapi
C 14	75.2	13.2	932	5	BX445843 BX445843
C 15	74.6	13.1	866	5	BX431776 BX431776
C 16	72.6	12.7	774	8	BZ135297 ZH85C09.1
C 17	71.4	12.5	548	1	AA001666 BF895306
C 18	68	11.9	511	2	BF895306 AG227224
C 19	65.8	11.5	455	8	BQ110978 HS 2017 B
C 20	65.8	11.5	964	4	BG110978 602284646
C 21	65	11.4	437	8	B54247 CIT-HSP-201
C 22	64	11.2	443	7	CF137776 UI-HF-BNO
C 23	63.8	11.2	470	5	BQ286427 1K30A01.Y
C 24	63.8	11.2	479	6	CB123801 K-EST0172

25	63.8	11.2	480	6	CB158377 K-EST0217
26	63.8	11.2	481	5	BO271452 1K14B03.Y
27	63.8	11.2	595	6	CA948940 i330C11.Y
28	63.8	11.2	641	5	B0951096 1075909.Y
C 29	63.8	11.2	733	6	CA307788 UI-H-FT1-
C 30	63.8	11.2	750	6	CA775717 1097410.X
C 31	63.8	11.2	752	6	CA775929 i01407.X
C 32	63.8	11.2	778	6	CA776003 1097410.Y
C 33	63.8	11.2	781	6	CA778017 i016N02.X
C 34	63.8	11.2	798	6	CA776148 i01407.Y
C 35	63.8	11.2	1042	4	BM474332 AGENCOURT
C 36	62.8	11.0	454	7	CN360600 170006001
C 37	62.2	10.9	711	6	CA778310 i016N02.Y
C 38	61.6	10.8	562	5	BO271156 1K14B03.X
C 39	61.6	10.8	593	5	BU076047 i053F11.X
C 40	61.6	10.8	601	5	BQ269772 1K30A01.X
C 41	61.6	10.8	615	5	B0952536 1075909.X
C 42	61.6	10.8	709	6	CD237377 FNPARD02
C 43	60.2	10.5	558	7	CK005159 AGENCOURT
C 44	60	10.5	712	1	AA875998 OB93B09.B
C 45	58.8	10.3	438	1	AI830973 wj80E03.X

## ALIGNMENTS

RESULT 1  
LOCUS AM593371 582 bp mRNA linear EST 22-MAR-2000  
DEFINITION hg13h11.x1 Soares NFL T GBC SI Homo sapiens CDNA clone  
IMAGE:2945541 3' similar to SW:VP40\_BDV Q01552 40 KD PROTEIN. [2]  
SW:VP40\_BDV / mRNA sequence.

ACCESSION AM593371.1 GI:7280629  
VERSION EST.  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL  
COMMENT Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-tr@mail.nih.gov

FEATURES  
source This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Seg primer: -40up from Gibco  
High quality sequence stop: 464.  
Location/Qualifiers

1..582  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2945541"  
/lab\_host="VDH10B"  
/clone\_jib="Soares NFL T GBC SI"  
/note="Organ: pooled; Vector: p773D-Pac (Pharmacia) with  
a modified polylinker; Site\_1: Not 1; Site\_2: Eco R1;  
Equal amounts of plasmid DNA from three normalized  
libraries (fetal lung Nhlh19W, testis NHR, and B-cell  
NCI CGAP GCBI) were mixed, and as circles were made in  
vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from pools of 5,000 clones made  
from the same 3 libraries. The pools consisted of  
1.M.A.G.E. clones 297480-302087, 682632-687239,  
726408-728711, and 729096-731399. Subtraction by Bento  
Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 15.6%; Score 88.8; DB 2; Length 582;

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OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 14:35:04 ; Search time 2798 Seconds

(without alignments)  
988.466 Million cell updates/sec

Title: US-10-627-141-16

Perfect score: 571  
Sequence: 1 TTCATACAGTAAGCCGACG.....CTTACATCCCTGTAAGTTC 571

Scoring table: IDENTITY\_NUC

Gapop 10.0 ; Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*  
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2: gb\_hig:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pal:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_scs:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	571	100.0	571	6	AR432670 Sequence
2	567.8	99.4	571	6	AR432668 Sequence
3	566.2	99.2	571	6	AR432669 Sequence
4	566.2	99.2	571	14	BDU58596
5	564.6	98.9	1112	6	AR098533 Sequence
6	564.6	98.9	1112	6	AR108878
7	564.6	98.9	8909	14	BD1311521
8	564.6	98.9	8910	6	AR098546
9	564.6	98.9	8910	6	AR108891
10	564.6	98.9	8910	14	BDU04608
11	563	98.6	571	14	BDU58594
12	561.4	98.3	571	14	BDU58595
13	561	98.2	8910	6	AR432655
14	560.6	98.2	571	6	AR432667
15	555	97.2	1110	14	BDU94867
16	553.4	96.9	8909	14	BDU311523
17	551.8	96.6	1110	14	BDU94863
18	551.8	96.6	3694	14	AY06023
19	540.6	94.7	1110	14	BDU94875

20	540.6	94.7	1110	14	BDU94879	U94879 Borna disea
21	540.6	94.7	1118	14	BDV38K	X68392 Borna disea
22	540.6	94.7	1133	14	BDV38K	M9375 Borna disea
23	540.6	94.7	1851	14	BDV38K	S62821 p38-putativ
24	540.6	94.7	8908	14	AY114161	AY114161 Borna dis
25	540.6	94.7	8908	14	AY114162	AY114162 Borna dis
26	540.6	94.7	8908	14	AY114163	AY114163 Borna dis
27	540.6	94.7	8908	14	BDV38K	L27077 Borna disea
28	540.6	94.7	8909	14	BDV38K	AF11522 Borna dis
29	537.4	94.1	1113	14	AF158629	AF158629 Borna dis
30	531	93.0	1138	14	SE750281	SE750281 Borna dis
31	529.4	92.7	1110	14	BDU94871	BDU94871 Borna disea
32	500.2	87.6	529	14	BD1246853	BD1246853 Borna dis
33	498.6	87.3	529	14	BD1246851	BD1246851 Borna dis
34	498.6	87.3	529	14	BD1246852	BD1246852 Borna dis
35	498.6	87.3	529	14	BD1246854	BD1246854 Borna dis
36	498.6	87.3	529	14	BD1246856	BD1246856 Borna dis
37	498.6	87.3	529	14	BD1246857	BD1246857 Borna dis
38	497	87.0	529	14	BDV38K	BDV38K Borna disea
39	493.8	86.5	529	14	BDV38K	BDV38K Borna disea
40	437.4	76.6	439	14	BDV38K	BDV38K Borna disea
41	434.2	76.0	439	14	BDV38K	BDV38K Borna disea
42	433.4	75.9	459	14	BDV38K	BDV38K Borna disea
43	432.6	75.8	439	14	BDV38K	BDV38K Borna disea
44	431	75.5	439	14	BDV38K	BDV38K Borna disea
45	431	75.5	439	14	BDV38K	BDV38K Borna disea

## ALIGNMENTS

RESULT 1	AR432670	Sequence 16 from patent US 6653464.	571 bp	mRNA	linear	PAT 18-DEC-2003
LOCUS	AR432670					
DEFINITION	Sequence 16 from patent US 6653464.					
ACCESSION	AR432670					
VERSION	AR432670.1	GI:40195249				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	Unclashed.					
AUTHORS	1 (bases 1 to 571)					
TITLE	de la Torre,J.C.					
JOURNAL	Methods and compositions for screening for human Borna disease					
FEATURES	Patent: US 6653464-A 16 25-NOV-2003;					
source	Location/Qualifiers					
ORIGIN	1..571					
	/organism="unknown"					
	/mol_type="mRNA"					

Query Match	100.0%	Score 571;	DB 6;	Length 571;	
Best Local Similarity	100.0%	Pred. No. 8.2e-175;			
Matches 571;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
1	TTCATACAGTAAGCCGACGCTTGTTCATATGTTGCTATATCCGAGTGCAGCGTG	60			
1	TTCATACAGTAAGCCGACGCTTGTTCATATGTTGCTATATCCGAGTGCAGCGTG	60			
1	TTCATACAGTAAGCCGACGCTTGTTCATATGTTGCTATATCCGAGTGCAGCGTG	60			
61	CGTTGTTACAGGAGGAGGCTGCTGATCTTACCTGACGCTTATCAGCGTGAG	120			
61	CGTTGTTACAGGAGGAGGCTGCTGATCTTACCTGACGCTTATCAGCGTGAG	120			
61	CGTTGTTACAGGAGGAGGCTGCTGATCTTACCTGACGCTTATCAGCGTGAG	120			
121	AACGAGCTGTTGTTAAACGAGGTTTAAAGGAGGAGGAGGAGGAGGAGGAGGAG	180			
121	AACGAGCTGTTGTTAAACGAGGTTTAAAGGAGGAGGAGGAGGAGGAGGAGGAG	180			
121	AACGAGCTGTTGTTAAACGAGGTTTAAAGGAGGAGGAGGAGGAGGAGGAGGAG	180			
181	CCGAGCTGAGAGATCTCTCTATCTTACGAGGATGTTGCTATTAAGGAGGAGGAG	240			
181	CCGAGCTGAGAGATCTCTCTATCTTACGAGGATGTTGCTATTAAGGAGGAGGAG	240			
181	CCGAGCTGAGAGATCTCTCTATCTTACGAGGATGTTGCTATTAAGGAGGAGGAG	240			
241	TAGGATGCTGCTTAAGATCAAAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	300			

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OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 11:37:54 ; Search time 422.333 Seconds  
(without alignments)  
8003.565 Million cell updates/sec

Title: US-10-627-141-16  
Perfect score: 571

Sequence: 1 TTCATCAGTACAGCCGAC.....CTTACATCCCTGTAAGTGC 571

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 segs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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1: geneeqn1980s:\*  
2: geneeqn1990s:\*  
3: geneeqn2000s:\*  
4: geneeqn2001as:\*  
5: geneeqn2001bs:\*  
6: geneeqn2002as:\*  
7: geneeqn2002bs:\*  
8: geneeqn2003as:\*  
9: geneeqn2003bs:\*  
10: geneeqn2003cs:\*  
11: geneeqn2003ds:\*  
12: geneeqn2004as:\*  
13: geneeqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	571	100.0	571	2	AAV32853
2	567.8	99.4	571	2	AAV32851
3	566.2	99.2	571	2	AAV32852
4	564.6	98.9	8910	2	AAV38104
5	537.4	94.1	1113	4	AAFe1225
6	448	78.5	559	4	AAFe1230
7	90.4	15.8	501	6	ABL36599
8	90.4	15.8	1047	4	AAH13875
9	90.4	15.8	1293	4	AAH161251
10	90.4	15.8	1293	10	ADBE08888
11	90	15.8	721	4	AAH04080
12	88.8	15.6	1311	10	ADBE07119
13	85.8	15.0	981	4	AAI59465
14	83.8	14.7	1626	12	AD000623
15	83.8	14.7	1626	12	AD000644
16	83.8	14.7	1626	12	AD000675
17	83.8	14.7	1626	12	AD000685
18	76.2	13.3	1665	10	AD053865
19	76.2	13.3	4940	10	ADFe82143
20	76.2	13.3	4940	10	ADFe82144

21	67.8	11.9	804	3	AACT7204
22	63.8	11.2	2843	4	AAH16588
23	60.6	10.6	712	6	ABT10107
24	58.6	10.3	430	10	ADFe80751
25	57.2	10.0	1557	12	AD084332
26	56.6	9.9	466	12	AD066154
27	56	9.8	767	4	AAI96380
28	45.8	8.0	836	4	AAI96519
29	38.6	6.8	2000	8	ADA71938
30	36	6.3	672	10	ADBS5214
31	36	6.3	672	10	ADBA9727
32	35.4	6.2	693	3	AAAT5126
33	33.8	5.9	250	3	AACT7230
34	33.8	5.9	553	4	AAH13122
35	33.8	5.9	35515	2	AAH20252
36	33.6	5.9	588	4	AAH09586
37	33.2	5.8	34980	5	AAFe6431
38	32.8	5.7	4983	12	AD063005
39	32.6	5.7	181257	12	ADFe69677
40	32.4	5.7	4062	8	ADA71340
41	32.4	5.7	5642	4	AAK69744
42	32.4	5.7	5642	5	AAK34694
43	32.2	5.6	883	2	AAK20351
44	32.2	5.6	110000	6	ABQ69245_16
45	32.2	5.6	110000	6	ABQ67195_1

## ALIGNMENTS

RESULT 1	AAV32853	AAV32853 standard; cDNA; 571 BP.
ID	AAV32853	
XX	XX	
AC	AAV32853;	
XX	XX	
DT	27-AUG-2003 (revised)	
DT	09-NOV-1998 (first entry)	
XX	XX	
DE	Human Borna disease virus p40 cDNA.	
XX	XX	
KW	BDV, infection; diagnosis; neuropsychiatric disorder; human; ss.	
XX	XX	
OS	Borna disease virus.	
XX	XX	
FH	Key	Location/Qualifiers
FT	CDS	3..569
FT		/*tag= a
XX	XX	
PN	WO9830238-A1.	
XX	XX	
PD	16-JUL-1998.	
XX	XX	
PF	07-JAN-1998;	98WO-US000495.
XX	XX	
PR	07-JAN-1997;	97US-00779764.
XX	XX	
PA	(SCRI ) SCRIPPS RES INST.	
XX	XX	
FI	De La Torre JC;	
XX	XX	
DR	WPI, 1998-398802/34.	
XX	XX	
DR	P-PSDB; AAM49053.	
XX	XX	
PT	New isolated human Borna disease nucleic acid(s) - which encode p24, p16, p56, p40 and L polymerase catalytic domain poly:peptide(s), used to develop products for detection.	
PT	Claim 15; Page 129; 207pp; English.	
XX	XX	
PS	This cDNA sequence codes for p40 polypeptide (see AAM49053) of a Borna disease virus (BDV) isolate (H3) obtained from a psychiatric patient with a mood disorder. It can be produced by PCR (see also AAV32866-69) of cDNA	
CC	CC	

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OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 14:41:19 ; Search time 130.667 Seconds  
(without alignments)  
7150.362 Million cell updates/sec

Title: US-10-627-141-16

Perfect score: 571

Sequence: 1 TTCTACAGTACAGCCGCCAGC.....CTTACATCCCTGTAGTTGC 571

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 105 summaries

Database :

Issued Patents NA: \*  
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3: /cgn2\_6/prodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/prodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/prodata/1/ina/PTUS COMB.seq.\*  
6: /cgn2\_6/prodata/1/ina/backfillseq.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	571	100.0	571	3	US-08-779-764A-16
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3	567.8	99.4	571	3	US-08-779-764A-14
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## ALIGNMENTS

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RESULT 1
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; Sequence 16, Application US/08779764A
; Patent No. 6057094
;
GENERAL INFORMATION:
; APPLICANT: de la Torre, Juan C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
; TITLE OF INVENTION: OF HUMAN BORNA DISEASE VIRUS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESS: THE SCRIPPS RESEARCH INSTITUTE
; STREET: 10550 No. 6057094th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: United States
; ZIP: 92037
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,764A
; FILING DATE: 16-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 465.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
;
US-08-779-764A-16
Query Match 100.0%; Score 571; DB 3; Length 571;
Best Local Similarity 100.0%; Pred. No. 6, 2e-193;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 17:28:54 ; Search time 463 Seconds

(Without alignments)  
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Title: US-10-627-141-16

Perfect score: 571

Sequence: 1 TTCACAGTAAGACCCAGC.....CTTACATCCCTTACTGTC 571

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Searched: 5607317 seqs, 302624599 residues

Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	567.8	99.4	571	US-10-627-141-14	Sequence 14, Appl
3	566.2	99.2	571	US-10-627-141-15	Sequence 15, Appl
4	561	98.2	8910	US-10-627-141-1	Sequence 1, Appl
5	560.6	98.2	571	US-10-627-141-13	Sequence 13, Appl
6	90.4	15.8	498	US-09-878-178-188	Sequence 188, App
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9	90.4	15.8	1293	US-10-126-558-288	Sequence 288, App
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C 15	57.2	10.0	1557	13	US-10-027-632-260704	Sequence 260704,
C 16	57.2	10.0	1557	13	US-10-027-632-260705	Sequence 260705,
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C 22	57.2	10.0	1557	17	US-10-027-632-260705	Sequence 260705,
C 23	57.2	10.0	1557	17	US-10-027-632-260706	Sequence 260706,
C 24	57.2	10.0	1557	17	US-10-027-632-260707	Sequence 260707,
C 25	57.2	10.0	1557	17	US-10-027-632-260708	Sequence 260708,
C 26	56.6	9.9	466	18	US-10-637-855-146	Sequence 146, App
C 27	34	6.0	121410	19	US-10-741-600-17733	Sequence 17733, A
C 28	33.4	5.8	305	17	US-10-242-535A-49642	Sequence 49642, A
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C 42	32.8	5.7	1323	13	US-10-027-632-251151	Sequence 251151,
C 43	32.8	5.7	1323	13	US-10-027-632-251151	Sequence 251151,
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#### ALIGNMENTS

##### RESULT 1

US-10-627-141-16

Sequence 16, Application US/10627141

Publication No. US20040162421A1

GENERAL INFORMATION:

APPLICANT: de la Torre, Juan C.

TITLE OF INVENTION: OF HUMAN BORNA DISEASE VIRUS

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE

STREET: 10550 North Torrey Pines Road, TPC-8

CITY: La Jolla

STATE: California

COUNTRY: United States

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/627,141

FILING DATE: 25-Jul-2003

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/779,764

FILING DATE: 16-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: TSRI 465.0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 784-2937

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

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Title: US-10-627-141-16

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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C 7	76.4	13.4	685	5	BQ006526 UI-H-EI1-
C 8	76.2	13.3	389	4	BM698664 UI-H-EI1-
C 9	76.2	13.3	500	1	AL599858 DKFZ313C
C 10	76.2	13.3	725	5	BQ183041 UI-H-EI1-
C 11	76.2	13.3	737	6	CB993540
C 12	76.2	13.3	1790	3	BC033624
C 13	76.2	13.3	1826	3	BC032471 Homo sapi
C 14	75.2	13.2	932	5	BM445843 BX445843
C 15	74.6	13.1	866	5	BX431776 BX431776
C 16	72.6	12.5	548	1	BZ135297 CH230-287
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C 18	69.6	12.2	511	2	BF895306
C 19	65.8	11.5	964	4	BG110978
C 20	64.2	11.2	455	4	AG227224 HS 2017.B
C 21	64	11.2	443	7	CF137776 UI-HF-BNO
C 22	63.8	11.2	479	6	BQ286427
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C 29	63.8	11.2	730	6	CA775717	CA775717 iQ97d10.x
C 30	63.8	11.2	752	6	CA775929	CA775929 iQ1d07.x
C 31	63.8	11.2	778	6	CA776003	CA776003 iQ97d10.Y
C 32	63.8	11.2	781	6	CA778017	CA778017 iQ16h02.x
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C 34	63.8	11.2	1042	4	BM474332	BM474332 AGENCOURT
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C 37	62.2	10.9	711	6	CA778310	CA778310 iQ16h02.Y
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C 44	60.2	10.5	558	7	CK005159	CK005159 AGENCOURT
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## ALIGNMENTS

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LOCUS  
DEFINITION  
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IMAGE:2945541 3' similar to SW:VP40\_BDV Q01552 40 KD PROTEIN. [2]  
SW:VP40\_BDV / mRNA sequence.

ACCESSION  
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VERSION  
AM593371.1 GI:7280629  
KEYWORDS  
EST.

SOURCE  
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ORGANISM  
Homo sapiens

REFERENCE  
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Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
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AUTHORS  
NCT-CGAP <http://www.ncbi.nlm.nih.gov/nctgap>.  
TITLE  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL  
Unpublished (1997)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapb-remail.nih.gov](mailto:cgapb-remail.nih.gov)  
This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Seq primer: -40UP from Gibco  
High quality sequence stop: 464.

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NCT CGAP (GCB) were mixed and as circles were made in  
vivo. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from pools of 5,000 clones made  
from the same 3 libraries. The pools consisted of  
I.M.A.G.E. clones 297480-302087, 682632-687239,  
726408-728711, and 729096-731399. Subtraction by Bento  
Soares and M. Fatima Bonaudo."

## ORIGIN

Query Match

15.8%; Score 90.4; DB 2; Length 582;